



SEQLIST.TXT

SEQUENCE LISTING

<110> Clontech Laboratories Inc.

<120> FAR RED SHIFTED FLUORESCENT PROTEINS

<130> CLON-028WO

<140> Unassigned

<141> 2001-10-12

<150> 60/240,018

<151> 2000-10-12

<150> 60,306,131

<151> 2001-07-16

<160> 28

<170> FastSEQ for Windows Version 4.0

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<211> 910

<212> DNA

<213> heteractis crispa

<400> 1

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ccatttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
gccttcgaca ttttggcacc gtgttgtagag tacggcagca ggacctttgt ccaccatacg 300
gcagagattc ccgatttcctt caagcagctt ttccctgaag gctttacttg ggaaagaacc 360
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<212> PRT

<213> heteractis crispa

<400> 2

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35     40     45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50     55     60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65     70     75     80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
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Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Cys	Thr		
	130					135					140						
Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met		
145					150					155					160		
Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	Leu	Tyr	Thr	Ser		
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Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His		
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Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Pro	Arg	Lys	Thr	Lys	Asp	Glu	Tyr		
		195					200					205					
Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu		
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Lys	Ala	Asn															
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<210> 3
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 <213> heteractis crispa

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<210> 4
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 <212> PRT
 <213> heteractis crispa

<400> 4

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			20					25					30		
Asn	Pro	Phe	Thr	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly
		35					40					45			
Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr
	50					55					60				
Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe
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Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
			85						90					95	
Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly

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Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala
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Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Glu	Gly	Trp	Glu	Pro	Cys	Thr
	130					135					140				
Glu	Val	Val	Tyr	Pro	Asp	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met
	145				150					155					160
Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	Leu	Tyr	Thr	Ser
			165						170					175	
Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His
		180						185					190		
Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Pro	Arg	Lys	Thr	Lys	Asp	Glu	Tyr
	195						200					205			
Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu
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Lys	Ala	Asn													
225															

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 <212> DNA
 <213> heteractis crispa

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 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
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 gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaatc aggaggatgg 420
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 gcccttaaag tcggtgatcg tcgtttgatc tgccatctct atacttctta caggtccaag 540
 aaagcagtcc gtgccttgac aatgccagga ttccatttta cagacatccg ccttcagatg 600
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<210> 6
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 <213> heteractis crispa

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		20						25					30		
Asn	Pro	Phe	Thr	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly
	35						40					45			
Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr
	50				55					60					
Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe
65				70					75					80	
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
		85						90					95		
Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly
		100						105					110		
Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala
	115						120					125			
Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr
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<213> heteractis crispa

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tgttgtgagt	acggcagcag	gacctttgtc	caccatacgg	cagagattcc	cgatttcttc	240
aagcagtctt	tccctgaagg	ctttacttgg	gaaagaacca	caacctatga	agatggaggc	300
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gtccttggtg	ccaattttcc	tgctgatggc	cccgtgatga	agaacaaatc	aggaggatgg	420
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gcccttaaag	tcggtgatcg	tcgtttgatc	tgccatcact	atacttctta	caggtccaag	540
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<210> 8
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<213> heteractis crispa

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	Asn	Pro	Phe	Ala	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly
	Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr
	Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe
65	Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
	Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly
	Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala
	Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr
	Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met
145	Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	His	Tyr	Thr	Ser
	Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His
	Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Leu	Arg	Lys	Glu	Lys	Asp	Glu	Tyr

SEQLIST.TXT

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210 215 220
Lys Ala Asn
225

<210> 9
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<212> DNA
<213> heteractis crispa

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tgttgtgctg acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
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gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
gcccttaaag tcggtgatcg tcgtttgatc tgccatcact atacttctta caggtccaag 540
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<212> PRT
<213> heteractis crispa

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35 40 45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr
50 55 60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65 70 75 80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100 105 110
Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
115 120 125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130 135 140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145 150 155 160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr
195 200 205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210 215 220
Lys Ala Asn
225

SEQLIST.TXT

<210> 11
 <211> 687
 <212> DNA
 <213> heteractis crispa

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 <213> heteractis crispa

<400> 12
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 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg His Leu Ile Cys His His Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
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<210> 13
 <211> 687
 <212> DNA
 <213> heteractis crispa

SEQLIST.TXT

<400> 13

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<210> 14

<211> 227

<212> PRT

<213> heteractis crispa

<400> 14

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20      25      30
Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35      40      45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50      55      60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65      70      75      80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85      90      95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100     105     110
Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
115     120     125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130     135     140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145     150     155     160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
165     170     175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180     185     190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr
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Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
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Lys Ala Asn
225

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<210> 15

<211> 1396

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion construct

<400> 15

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SEQLIST.TXT

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cgcccaccag gacaccagcc tggagggcaa ctgcctgatc tacaagggtga aggtgctggg 1080
caccaacttc cccgccgacg gccccgtgat gaagaacaag agcggcggct gggagcccag 1140
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ggtgggcgac cggcggctga tctgccacca ctacaccagc taccggagca agaaggccgt 1260
gcggggcctg accatgcccg gcttccactt caccgacatc cggctgcaga tgctgcggaa 1320
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<210> 16

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion construct

<400> 16

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          20          25          30
Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
          35          40          45
Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
          50          55          60
Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
65          70          75          80
Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
          85          90          95
Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
          100          105          110
Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
          115          120          125
Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
130          135          140
Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
145          150          155          160
Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
          165          170          175
Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
          180          185          190
His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
          195          200          205
Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
210          215          220
Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu
225          230          235          240
Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr

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SEQLIST.TXT

Phe	Lys	Cys	Glu	245	Gly	Glu	Gly	Asp	Gly	250	Asn	Pro	Phe	Ala	Gly	255	Thr	Gln
Ser	Met	Arg	Ile	260	His	Val	Thr	Glu	Gly	265	Ala	Pro	Leu	Pro	Phe	270	Ala	Phe
Asp	Ile	Leu	Ala	275	Pro	Cys	Cys	Glu	Tyr	280	Gly	Ser	Arg	Thr	Phe	285	Val	His
His	Thr	Ala	Glu	290	Ile	Pro	Asp	Phe	Phe	295	Lys	Gln	Ser	Phe	Pro	Glu	Gly	300
305	Thr	Trp	Glu	310	Arg	Thr	Thr	Thr	Tyr	315	Glu	Asp	Gly	Gly	Ile	Leu	Thr	320
Phe	Thr	Trp	Glu	325	Thr	Ser	Leu	Glu	Gly	330	Asn	Cys	Leu	Ile	Tyr	Lys	Val	335
Ala	His	Gln	Asp	340	Thr	Asn	Phe	Pro	Ala	345	Asp	Gly	Pro	Val	Met	Lys	Asn	350
Lys	Val	Leu	Gly	355	Thr	Asn	Phe	Pro	Ala	360	Asp	Gly	Pro	Val	Met	Lys	Asn	365
Lys	Ser	Gly	Gly	370	Trp	Glu	Pro	Ser	Thr	375	Glu	Val	Val	Tyr	Pro	Glu	Asn	380
Gly	Val	Leu	Cys	385	Gly	Arg	Asn	Val	Met	390	Ala	Leu	Lys	Val	Gly	Asp	Arg	400
Arg	Leu	Ile	Cys	405	His	His	Tyr	Thr	Ser	410	Tyr	Arg	Ser	Lys	Lys	Ala	Val	415
Arg	Ala	Leu	Thr	420	Met	Pro	Gly	Phe	His	425	Phe	Thr	Asp	Ile	Arg	Leu	Gln	430
Met	Leu	Arg	Lys	435	Glu	Lys	Asp	Glu	Tyr	440	Phe	Glu	Leu	Tyr	Glu	Ala	Ser	445
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<210> 17
 <211> 1424
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 17

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cgccggcacc	cagagcatgc	ggatccacgt	gaccgagggc	gccccctgc	ccttcgcctt	180
cgacatcctg	gccccctgct	gcgagtacgg	cagcaggacc	ttcgtgcacc	acaccgccga	240
gatccccgac	ttcttcaagc	agagcttccc	cgagggcttc	acctgggaga	gaaccaccac	300
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gatctacaag	gtgaaggtgc	tgggcaccaa	cttccccgcc	gacggccccg	tgatgaagaa	420
caagagcggc	ggctgggagc	ccagcaccga	ggtggtgtac	cccagagaacg	gcgtgctgtg	480
cggccggaac	gtgatggccc	tgaaggtggg	cgaccggcgg	ctgatctgcc	accactacac	540
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catccggctg	cagatgctgc	ggaaggagaa	ggacgagtac	ttcgagctgt	acgaggccag	660
cgtggcccgg	tacagcgacc	tgcccagaaa	ggccaacaga	tctcccggga	tggtgagcgg	720
cctgctgaag	gagagcatgc	gcatcaagat	gtacatggag	ggcaccgtga	acggccacta	780
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gcggggccctg	accatgcccg	gcttccactt	caccgacatc	cggtgcaga	tgctgcggaa	1320
ggagaaggac	gagtacttcg	agctgtacga	ggccagcgtg	gcccgggtaca	gcgacctgcc	1380
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<210> 18
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 18
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 35 40 45
 Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
 50 55 60
 Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
 65 70 75 80
 Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
 85 90 95
 Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
 100 105 110
 Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
 115 120 125
 Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
 130 135 140
 Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
 145 150 155 160
 Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
 165 170 175
 Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
 180 185 190
 His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
 195 200 205
 Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
 210 215 220
 Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu
 225 230 235 240
 Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr
 245 250 255
 Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln
 260 265 270
 Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe
 275 280 285
 Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His
 290 295 300
 His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly
 305 310 315 320
 Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr
 325 330 335
 Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val
 340 345 350
 Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn
 355 360 365
 Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn
 370 375 380
 Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg
 385 390 395 400
 Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val
 405 410 415
 Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln
 420 425 430

SEQLIST.TXT

Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser
 435 440 445
 Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn Arg Thr Arg Ala
 450 455 460
 Met Asp Asp Asp Ile Ala
 465 470

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 19
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27

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 20
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21

<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 21
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21

<210> 22
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 22
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<210> 23
 <211> 684
 <212> DNA
 <213> heteractis crispa

<400> 23
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 atgaggattc atgtcaccga aggggctcca ttaccatttg ctttcgacat tttggcaccg 180
 tggtgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300

SEQLIST.TXT

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gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
gcccttaaag tcggtgatcg tcgtttgatc tgccatctct atactttcta caggtccaag 540
aaagcagtcc gtgccttgac aatgccagga ttcatcttta cagacatccg ccttcagatg 600
ccgaggaaaa agaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
gatcttcctg aaaaagcaaa ttga 684
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<210> 24
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 24
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 20 25 30
 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Lys Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 25
 <211> 683
 <212> DNA
 <213> heteractis crispa

<400> 25
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 atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
 tggtgtgctg acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
 attcttactg ctcacagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
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 agccaagcac tgaggtggtt tatccagaga atggtgtcct gtgtggacgt aatgtgatgg 480
 cccttaaagt cggtgatcgt cgtttgatct gccatcacta tacttcttac aggtccaaga 540
 aagcagtccg tgccttgaca atgccaggat ttcatctttac agacatccgc cttcagatgc 600
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<210> 26
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 26
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 20 25 30
 Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Lys Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 27
 <211> 910
 <212> DNA
 <213> heteractis crispa

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 tacatggaag gcacgggttaa tggccattat ttcaagtgtg aaggagaggg agacggcaac 180
 ccatttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
 gccttcgaca ttttggcacc gtgttggtgag tacggcagca ggacctttgt ccaccatacg 300
 gcagagattc ccgatttcctt caagcagtct ttccctgaag gctttacttg ggaaagaacc 360
 acaacctatg aagatggagg cattcttact gctcatcagg acacaagcct ggaggggaac 420
 tgccttatat acaaggtgaa agtccttggt accaattttc ctgctgatgg ccccgatgat 480
 aagaacaaat caggaggatg ggagccatgc actgaggtgg tttatccaga gaatggtgtc 540
 ctgtgtggac gtaatgtgat ggcccttaaa gtcggtgatc gtcgtttgat ctgccatctc 600
 tatacttctt acaggtccaa gaaagcagtc cgtgccttga caatgccagg atttcatttt 660
 acagacatcc gccttcagat gccgaggaaa acgaaagacg agtactttga actgtacgaa 720
 gcatctgtgg ctaggtacag tgatcttcct gaaaaagcaa attgattgtt cccagtgaca 780
 ccagactgct gtcagctttt ggttaaagcc cgaaagacaa aaggacattt gtagtttagt 840
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 cattaacct 910

SEQLIST.TXT

<210> 28
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 28

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			20					25					30		
Asn	Pro	Phe	Thr	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly
		35					40					45			
Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr
	50					55					60				
Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe
65					70					75					80
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
				85					90					95	
Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly
			100					105					110		
Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala
		115					120					125			
Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Cys	Thr
	130					135					140				
Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met
145					150					155					160
Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	Leu	Tyr	Thr	Ser
				165					170					175	
Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His
			180					185					190		
Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Pro	Arg	Lys	Thr	Lys	Asp	Glu	Tyr
		195					200					205			
Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu
	210					215					220				
Lys	Ala	Asn													
225															